



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/446,089E

DATE: 07/26/2004
TIME: 11:26:58

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF4\07262004\I446089E.raw

4 <110> APPLICANT: SAKAKIBARA, Keiko
5 FUKUI, Yuko
6 TANAKA, Yoshikazu
7 KUSUMI, Takaaki
8 MIZUTANI, Masako
9 NAKAYAMA, Toru
11 <120> TITLE OF INVENTION: GENE ENCODING PROTEIN HAVING AURONE SYNTHESIZING ACTIVITY
13 <130> FILE REFERENCE: 001560-377
15 <140> CURRENT APPLICATION NUMBER: US 09/446,089E
16 <141> CURRENT FILING DATE: 1999-12-17
18 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02045
19 <151> PRIOR FILING DATE: 1999-04-16
21 <150> PRIOR APPLICATION NUMBER: JP 10/107296
22 <151> PRIOR FILING DATE: 1998-04-17
24 <160> NUMBER OF SEQ ID NOS: 15
26 <170> SOFTWARE: PatentIn version 3.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1951
30 <212> TYPE: DNA
31 <213> ORGANISM: Antirrhinum majus
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (96)..(1781)
37 <400> SEQUENCE: 1
38 aaattacatt gttccctttg tcccaccttc caccaccaat atatacaact tcctcagcta 60
40 gttgtttatt atcaatcaaa taaaattatt tccca atg ttc aaa aat cct aat 113
41 Met Phe Lys Asn Pro Asn
42 1 5
44 atc cgc tat cac aaa cta tct tcc aaa tcc aat gac aac gat caa gaa 161
45 Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Gln Glu
46 10 15 20
48 tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc 209
49 Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe
50 25 30 35
52 cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc cgg 257
53 Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg
54 40 45 50
56 ttt gcc tcg acc tca acc ggc cct atc gcc gcc cct gat gtc acc aaa 305
57 Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys
58 55 60 65 70
60 tgt ggt cag cca gac ttg cca cct ggc aca gcc cca ata aac tgt tgt 353
61 Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys
62 75 80 85



P.b

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| | |
|---|------|
| 64 ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc | 401 |
| 65 Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser | |
| 66 90 95 100 | |
| 68 act acc atg agg gtt cgc cgt gct cat tta gtt gat gat gca tac | 449 |
| 69 Thr Thr Met Arg Val Arg Arg Ala Ala His Leu Val Asp Asp Ala Tyr | |
| 70 105 110 115 | |
| 72 att gcc aaa ttc aag aaa gcc gtt gag ctt atg cga gct cta cct gag | 497 |
| 73 Ile Ala Lys Phe Lys Lys Ala Val Glu Leu Met Arg Ala Leu Pro Glu | |
| 74 120 125 130 | |
| 76 gat gac cct cgt agc ttc aag caa gct aac gtc cat tgc gct tac | 545 |
| 77 Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr | |
| 78 135 140 145 150 | |
| 80 tgc gcg ggg gcg tat aat caa gcc ggt ttc aca aac cta aag ctc caa | 593 |
| 81 Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln | |
| 82 155 160 165 | |
| 84 atc cac cga tct tgg ctt ttt ttc ccg ttc cat aga tat tat atc tac | 641 |
| 85 Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr | |
| 86 170 175 180 | |
| 88 ttt ttt gaa aga ata ttg gga aaa cta atc aat gat aca act ttt gct | 689 |
| 89 Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala | |
| 90 185 190 195 | |
| 92 ctc caa ttt tgg aac tat gat tca cct ggt gga atg aca atc cca tca | 737 |
| 93 Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser | |
| 94 200 205 210 | |
| 96 atg ttt att gat act aat tct tcg ctg tac gat agt tta cgg gac agt | 785 |
| 97 Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser | |
| 98 215 220 225 230 | |
| 100 aat cat cag cca cca acc atc gta gac ttg aac tac gcc ttt tct gat | 833 |
| 101 Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp | |
| 102 235 240 245 | |
| 104 tcc gac aat acc act act cct gaa gag caa atg att ata aac ctt aaa | 881 |
| 105 Ser Asp Asn Thr Thr Pro Glu Glu Gln Met Ile Ile Asn Leu Lys | |
| 106 250 255 260 | |
| 108 att gtg tac aga caa atg gtg tcg agc gct aag act cca cag ctt ttc | 929 |
| 109 Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe | |
| 110 265 270 275 | |
| 112 ttc ggc cgc cca tac cga cgt ggg gac caa gag ttt ccc ggg gtg ggg | 977 |
| 113 Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly | |
| 114 280 285 290 | |
| 116 tcg att gag tta gtc cct cat ggc atg ata cat tta tgg acc ggt tct | 1025 |
| 117 Ser Ile Glu Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser | |
| 118 295 300 305 310 | |
| 120 gag aac acg ccc tat ggc gag aac atg ggg gct ttc tac tca acg gct | 1073 |
| 121 Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala | |
| 122 315 320 325 | |
| 124 aga gac ccg ata ttt ttt gct cat cat tcg aac gtc gat aga atg tgg | 1121 |
| 125 Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp | |
| 126 330 335 340 | |
| 128 tcc ata tgg aag acc cta gga ggg ccg cgg agg acg gac tta aca gat | 1169 |

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129 Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp
130      345      350      355
132 cca gat ttt ctt gat gcg tct ttc gtt ttt tat gac gaa aac gca gag      1217
133 Pro Asp Phe Leu Asp Ala Ser Phe Val Phe Tyr Asp Glu Asn Ala Glu
134      360      365      370
136 atg gtt cgg gtc aag gtt cggt gat tgc tta gat gaa aag aaa cta ggg      1265
137 Met Val Arg Val Lys Val Arg Asp Cys Leu Asp Glu Lys Lys Leu Gly
138 375      380      385      390
140 tac gtt tat caa gat gtg gag att ccg tgg ctc aac act cgt cca aca      1313
141 Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp Leu Asn Thr Arg Pro Thr
142      395      400      405
144 cca aaa gtt tct ccg tct cta ctt aag aaa ttt cat aga aca aac act      1361
145 Pro Lys Val Ser Pro Ser Leu Leu Lys Lys Phe His Arg Thr Asn Thr
146      410      415      420
148 gcc aat ccg aga caa gtt ttt cct gcg ata ctt gac aga gtc tta aaa      1409
149 Ala Asn Pro Arg Gln Val Phe Pro Ala Ile Leu Asp Arg Val Leu Lys
150      425      430      435
152 gtt atc gtg acg agg ccg aag aaa act aga agt agg aaa gaa aag gac      1457
153 Val Ile Val Thr Arg Pro Lys Lys Thr Arg Ser Arg Lys Glu Lys Asp
154      440      445      450
156 gag tta gaa gag att tta gtg att gaa ggg att gaa ctg gaa aga gac      1505
157 Glu Leu Glu Glu Ile Leu Val Ile Glu Gly Ile Glu Leu Glu Arg Asp
158 455      460      465      470
160 cac ggg cac gta aaa ttc gac gtt tat att aat gct gac gaa gat gac      1553
161 His Gly His Val Lys Phe Asp Val Tyr Ile Asn Ala Asp Glu Asp Asp
162      475      480      485
164 ctt gcg gtg att tcg ccg gag aat gct gag ttc gcc ggg agt ttc gtg      1601
165 Leu Ala Val Ile Ser Pro Glu Asn Ala Glu Phe Ala Gly Ser Phe Val
166      490      495      500
168 agt ctg tgg cac aaa cct ata aag ggg aag agg aca aag acg cag tta      1649
169 Ser Leu Trp His Lys Pro Ile Lys Gly Lys Arg Thr Lys Thr Gln Leu
170      505      510      515
172 tta aca ttg tcg att tgt gat att ttg gag gat ttg gat gct gac gaa      1697
173 Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu Asp Leu Asp Ala Asp Glu
174      520      525      530
176 gat gat tat gtg ttg gtc act ttg gtt ccg aga aac gcc gga gat gcg      1745
177 Asp Asp Tyr Val Leu Val Thr Leu Val Pro Arg Asn Ala Gly Asp Ala
178 535      540      545      550
180 atc aag att cat aat gtc aag att gag ctt gat ggc taataaaattc      1791
181 Ile Lys Ile His Asn Val Lys Ile Glu Leu Asp Gly
182      555      560
184 tattgatttc ttctcaacct acagttgatc atttaccat tgattattcc aataaaagta      1851
186 tctcatgtac caatatcgat cgtattaatc gtaatacttt cagattttta tttattnaa      1911
188 agcagttgta taaatggta aataaggatt acttttgag      1951
192 <210> SEQ ID NO: 2
193 <211> LENGTH: 562
194 <212> TYPE: PRT
195 <213> ORGANISM: Antirrhinum majus
197 <400> SEQUENCE: 2
  
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199 Met Phe Lys Asn Pro Asn Ile Arg Tyr His Lys Leu Ser Ser Lys Ser
200 1 5 10 15
203 Asn Asp Asn Asp Gln Glu Ser Ser His Arg Cys Lys His Ile Leu Leu
204 20 25 30
207 Phe Ile Ile Thr Leu Phe Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn
208 35 40 45
211 Ser Leu Ala Tyr Ala Arg Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala
212 50 55 60
215 Ala Pro Asp Val Thr Lys Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr
216 65 70 75 80
219 Ala Pro Ile Asn Cys Cys Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe
220 85 90 95
223 Glu Leu Pro Pro Pro Ser Thr Thr Met Arg Val Arg Arg Ala Ala His
224 100 105 110
227 Leu Val Asp Asp Ala Tyr Ile Ala Lys Phe Lys Lys Ala Val Glu Leu
228 115 120 125
231 Met Arg Ala Leu Pro Glu Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala
232 130 135 140
235 Asn Val His Cys Ala Tyr Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe
236 145 150 155 160
239 Thr Asn Leu Lys Leu Gln Ile His Arg Ser Trp Leu Phe Phe Pro Phe
240 165 170 175
243 His Arg Tyr Tyr Ile Tyr Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile
244 180 185 190
247 Asn Asp Thr Thr Phe Ala Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly
248 195 200 205
251 Gly Met Thr Ile Pro Ser Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr
252 210 215 220
255 Asp Ser Leu Arg Asp Ser Asn His Gln Pro Pro Thr Ile Val Asp Leu
256 225 230 235 240
259 Asn Tyr Ala Phe Ser Asp Ser Asp Asn Thr Thr Pro Glu Glu Gln
260 245 250 255
263 Met Ile Ile Asn Leu Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala
264 260 265 270
267 Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
268 275 280 285
271 Glu Phe Pro Gly Val Gly Ser Ile Glu Leu Val Pro His Gly Met Ile
272 290 295 300
275 His Leu Trp Thr Gly Ser Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly
276 305 310 315 320
279 Ala Phe Tyr Ser Thr Ala Arg Asp Pro Ile Phe Phe Ala His His Ser
280 325 330 335
283 Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg
284 340 345 350
287 Arg Thr Asp Leu Thr Asp Pro Asp Phe Leu Asp Ala Ser Phe Val Phe
288 355 360 365
291 Tyr Asp Glu Asn Ala Glu Met Val Arg Val Lys Val Arg Asp Cys Leu
292 370 375 380
295 Asp Glu Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp

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296 385 390 395 400
 299 Leu Asn Thr Arg Pro Thr Pro Lys Val Ser Pro Ser Leu Leu Lys Lys
 300 405 410 415
 303 Phe His Arg Thr Asn Thr Ala Asn Pro Arg Gln Val Phe Pro Ala Ile
 304 420 425 430
 307 Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg
 308 435 440 445
 311 Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly
 312 450 455 460
 315 Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile
 316 465 470 475 480
 319 Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu
 320 485 490 495
 323 Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys
 324 500 505 510
 327 Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu
 328 515 520 525
 331 Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro
 332 530 535 540
 335 Arg Asn Ala Gly Asp Ala Ile Lys Ile His Asn Val Lys Ile Glu Leu
 336 545 550 555 560
 339 Asp Gly
 342 <210> SEQ ID NO: 3
 343 <211> LENGTH: 13
 344 <212> TYPE: PRT
 345 <213> ORGANISM: Antirrhinum majus
 347 <400> SEQUENCE: 3
 349 Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro
 350 1 5 10
 353 <210> SEQ ID NO: 4
 354 <211> LENGTH: 12
 355 <212> TYPE: PRT
 356 <213> ORGANISM: Antirrhinum majus
 358 <400> SEQUENCE: 4
 360 Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys
 361 1 5 10
 364 <210> SEQ ID NO: 5
 365 <211> LENGTH: 18
 366 <212> TYPE: PRT
 367 <213> ORGANISM: Antirrhinum majus
 369 <400> SEQUENCE: 5
 371 Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
 372 1 5 10 15
 374 Glu Phe
 377 <210> SEQ ID NO: 6
 378 <211> LENGTH: 30
 379 <212> TYPE: PRT
 380 <213> ORGANISM: Antirrhinum majus
 382 <220> FEATURE:

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/26/2004
PATENT APPLICATION: US/09/446,089E TIME: 11:26:59

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF4\07262004\I446089E.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 9,29
Seq#:8; Xaa Pos. 2
Seq#:9; Xaa Pos. 6
Seq#:11; N Pos. 6,15,18
Seq#:12; N Pos. 12
Seq#:13; N Pos. 4,7

VERIFICATION SUMMARY DATE: 07/26/2004
PATENT APPLICATION: US/09/446,089E TIME: 11:26:59

Input Set : A:\001560-377.ST25.txt
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L:394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
M:341 Repeated in SeqNo=6
L:448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:538 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0